AMENDMENTS TO THE CLAIMS

1. - 35. (canceled)

36. (currently amended) A method of identifying a human having an increased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) ~~in said human's nucleic acids as shown by~~ at position 101 of SEQ ID NO: 5502 or its complement, wherein a G/G genotype at position 101 of SEQ ID NO:5502 or a C/C genotype at position 101 of its complement indicates said human has ~~the presence of C or its complement at the SNP is indicative of~~ an increased risk for developing RF+ RA ~~in said human~~.

37. - 38. (canceled)

39. (previously presented) The method of claim 36 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

40. (previously presented) The method of claim 36 in which the SNP is located at position 6497 of SEQ ID NO: 1688.

41. (currently amended) The method of claim 36 in which said nucleic acid is a nucleic acid extract ~~human's nucleic acids are extracted~~ from a biological sample of said human.

42. (currently amended) The method of claim 41 in which said biological sample is blood, saliva, or buccal cells.

43. (currently amended) The method of claim 36, wherein said testing step comprises nucleic acid amplification ~~in which said human's nucleic acids are amplified before the identity of the SNP is determined~~.

44. (currently amended) The method of claim 36 in which the testing is performed ~~identity of the SNP is determined~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

45. (currently amended) The method of claim 36 in which the testing is performed ~~identity of the SNP is determined~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

46. - 55. (canceled)

56. (currently amended) A method of determining a human's risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) ~~in said human's nucleic acids as shown by~~ at position 101 of SEQ ID NO: 5502 or its complement, wherein a G/G genotype at position 101 of SEQ ID NO:5502 or a C/C genotype at position 101 of its complement indicates said human has ~~the presence of C or its complement at the SNP is indicative of~~ an increased risk for developing RF+ RA ~~in said human~~, or A at position 101 of SEQ ID NO:5502 or T at its complement indicates said human has ~~, the presence of T or its complement at the SNP is indicative of~~ a decreased risk for developing RF+ RA ~~in said human~~.

57. - 58. (canceled)

59. (previously presented) The method of claim 56 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

60. (previously presented) The method of claim 56 in which the SNP is located at position 6497 of SEQ ID NO: 1688.

61. (currently amended) The method of claim 56 in which said nucleic acid is a nucleic acid extract ~~human's nucleic acids are extracted~~ from a biological sample of said human.

62. (currently amended) The method of claim 61 in which said biological sample is blood, saliva, or buccal cells.

63. (currently amended) The method of claim 56, wherein said testing step comprises nucleic acid amplification ~~in which said human's nucleic acids are amplified before the identity of the SNP is determined~~.

64. (currently amended) The method of claim 56 in which the testing is performed ~~identity of the SNP is determined~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

65. (currently amended) The method of claim 56 in which the testing is performed ~~identity of the SNP is determined~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

66. (currently amended) A method of identifying a human having a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) ~~in said human's nucleic acids as shown by~~ at position 101 of SEQ ID NO: 5502 or its complement, wherein A at position 101 of SEQ ID NO:5502 or T at its complement indicates said human has ~~the presence of T or its complement at the SNP is indicative of~~ a decreased risk for developing RF+ RA ~~in said human~~.

67. (previously presented) The method of claim 66 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

68. (previously presented) The method of claim 66 in which the SNP is located at position 6497 of SEQ ID NO: 1688.

69. (currently amended) The method of claim 66 in which said nucleic acid is a nucleic acid extract ~~human's nucleic acids are extracted~~ from a biological sample of said human.

70. (currently amended) The method of claim 69 in which said biological sample is blood, saliva, or buccal cells.

71. (currently amended) The method of claim 66, wherein said testing step comprises nucleic acid amplification ~~in which said human's nucleic acids are amplified before the identity of the SNP is determined~~.

72. (currently amended) The method of claim 66 in which the testing is performed ~~identity of the SNP is determined~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

73. (currently amended) The method of claim 66 in which the testing is performed ~~identity of the SNP is determined~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

74. (currently amended) A method of identifying a human having a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human for the presence or absence of ~~determining the identity of the~~ single nucleotide polymorphism (SNP) hCV163035 ~~rs2276864 in said human's nucleic acids~~, wherein A at the SNP based on the sequence orientation of SEQ ID NO:5502 or T at the SNP based on the sequence orientation of the complement of SEQ ID NO:5502 indicates said human has ~~the presence of T or its complement at the SNP is indicative of~~ a decreased risk for developing RF+ RA ~~in said human~~.

75. (new) A method of identifying a human having a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human for the presence or absence of single nucleotide polymorphism (SNP) hCV163035, wherein a G/G genotype at the SNP based on the sequence orientation of SEQ ID NO:5502 or a C/C genotype at the SNP based on the sequence orientation of the complement of SEQ ID NO:5502 indicates said human has an increased risk for developing RF+ RA.

76. (new) The method of claim 61, further comprising preparing said nucleic acid extract from said biological sample prior to said testing step.

77. (new) The method of claim 76, further comprising obtaining said biological sample from said human prior to said preparing step.

78. (new) The method of claim 63, wherein said nucleic acid amplification is carried out by polymerase chain reaction.

79. (new) The method of claim 36, further comprising correlating the presence of said G/G genotype or said C/C genotype with an increased risk for developing coronary stenosis.

80. (new) The method of claim 79, wherein said correlating step is performed by computer software.

81. (new) The method of claim 36, further comprising correlating the absence of said G/G genotype or said C/C genotype with no increased risk for developing coronary stenosis.

82. (new) The method of claim 81, wherein said correlating step is performed by computer software.

83. (new) The method of claim 66, further comprising correlating the presence of said A or said T with a decreased risk for developing coronary stenosis.

84. (new) The method of claim 83, wherein said correlating step is performed by computer software.